

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hillman, Jennifer L.  
Goli, Surya K.

(ii) TITLE OF THE INVENTION: NOVEL MICROTUBULE-ASSOCIATED PROTEIN

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.  
(B) STREET: 3174 Porter Drive  
(C) CITY: Palo Alto  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned  
(B) FILING DATE: Herewith  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.  
(B) REGISTRATION NUMBER: 36,749  
(C) REFERENCE/DOCKET NUMBER: PF-0211 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415-855-0555  
(B) TELEFAX: 415-845-4166  
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: THYRNOT03  
(B) CLONE: 144378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

092040603 - 071201

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Ser | Asp | Arg | Pro | Phe | Lys | Gln | Arg | Arg | Ser | Phe | Ala | Asp | Arg |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Cys | Lys | Glu | Val | Gln | Gln | Ile | Arg | Asp | Gln | His | Pro | Ser | Lys | Ile | Pro |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Ile | Ile | Glu | Arg | Tyr | Lys | Gly | Glu | Lys | Gln | Leu | Pro | Val | Leu | Asp |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Lys | Thr | Lys | Phe | Leu | Val | Pro | Asp | His | Val | Asn | Met | Ser | Glu | Leu | Val |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Lys | Ile | Ile | Arg | Arg | Arg | Leu | Gln | Leu | Asn | Pro | Thr | Gln | Ala | Phe | Phe |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     |     | 75  |     | 80  |
| Leu | Leu | Val | Asn | Gln | His | Ser | Met | Val | Ser | Val | Ser | Thr | Pro | Ile | Ala |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asp | Ile | Tyr | Glu | Gln | Glu | Lys | Asp | Glu | Asp | Gly | Phe | Leu | Tyr | Met | Val |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Ala | Ser | Gln | Glu | Thr | Phe | Gly | Phe |     |     |     |     |     |     |     |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THYRNOT03
- (B) CLONE: 1441378

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

|            |             |            |            |             |            |     |
|------------|-------------|------------|------------|-------------|------------|-----|
| CTCCCGCAGC | CCCAGCCGCC  | GTGCTCAGCG | CGAGCCCCGG | AGCCCTTGAG  | CGCGAGGC   | 60  |
| GGAGCCCCGG | AGCCCCCAA   | CCGAGAACAC | ATCCCCGCGC | CCAGAGCCC   | CGCCCTGCGC | 120 |
| GCCCCGGG   | GCCCCGGG    | TGCCCTCAGA | TGGCCCTTTA | AAGCAGCGC   | GGAGCTTCGC | 180 |
| CGACCGCTGT | AAGGAGGTAC  | AGCAGATCGG | CGACCAGCAC | CCCAGCAAA   | TCCCCGGTAT | 240 |
| CATCGAGCGC | TACAAGGGTG  | AGAACGACT  | GGCCGTCTTG | GACAAGACCA  | AGTTTTGGT  | 300 |
| CCCGGACCAT | GTCAACATGA  | GGCAGTTGGT | CAAGATCATC | CGGGGCCGCC  | TGCAGCTGAA | 360 |
| CCCCAGCGA  | GCCCTCTTCC  | TGCTGTGAA  | CCAGCACAGC | ATGGTGAGTG  | TGTCACGCC  | 420 |
| CATCGGGAC  | ATCTACGAGC  | TACAAGAAA  | CGAGGACCGC | TTCCCTCTATA | TGGCTCTAGC | 480 |
| CTCCCAGGAA | ACCTTCGGCT  | TCTGAGCCAG | CAGTAGGGGG | GCTGGCCCTG  | GGAGTCGGG  | 540 |
| GGCCCGGGTC | AGGCCCTGCC  | CAGAGAGCTT | CTGGTTCTGT | AACTGAGCTG  | CCTCTACCGT | 600 |
| GGTGGGCTGG | CGAGGCGATGT | GCCCGGATAG | TCAAGAGGCC |             |            | 640 |

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 455109

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Ser | Glu | Lys | Thr | Phe | Lys | Gln | Arg | Arg | Ser | Phe | Glu | Gln | Arg |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Val | Glu | Asp | Val | Arg | Leu | Ile | Arg | Glu | Gln | His | Pro | Thr | Lys | Ile | Pro |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |

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Val Ile Ile Glu Arg Tyr Lys Gly Glu Lys Gln Leu Pro Val Leu Asp  
35 40 45  
Lys Thr Lys Phe Leu Val Pro Asp His Val Asn Met Ser Glu Leu Ile  
50 55 60  
Lys Ile Ile Arg Arg Arg Leu Gln Leu Asn Ala Asn Gln Ala Phe Phe  
65 70 75 80  
Leu Leu Val Asn Gly His Ser Met Val Ser Val Ser Thr Pro Ile Ser  
85 90 95  
Glu Val Tyr Glu Ser Glu Arg Asp Glu Asp Gly Phe Leu Tyr Met Val  
100 105 110  
Tyr Ala Ser Gln Glu Thr Phe Gly Thr Ala Leu Ala Val Thr Tyr Met  
115 120 125  
Ser Ala Leu Lys Ala Thr Ala Thr Gly Arg Glu Pro Cys Leu  
130 135 140

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